

SEQUENCE LISTING

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<120> SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)

<130> 28967/35255A

<140>

<141>

<150> PCT/US99/06133

<151> 1999-03-26

<160> 28

<170> PatentIn Ver. 2.0

<210> 1

<211> 4111

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (20)..(4111)

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<223> Human Flt4 (VEGFR-3) long form cDNA

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007549-034600

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003443-03450

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Pro	Arg	Val	Ala	Pro 645	Glu	His	Glu	Gly	His 650	Tyr	Val	Cys	Glu	Val 655	Gln
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Tyr	Asp	Ala 835	Ser	Gln	Trp	Glu	Phe 840	Pro	Arg	Glu	Arg 845	Leu	His	Leu	Gly
Arg 850	Val	Leu	Gly	Tyr	Gly	Ala 855	Phe	Gly	Lys	Val 860	Val	Glu	Ala	Ser	Ala
Phe 865	Gly	Ile	His	Lys 870	Gly	Ser	Ser	Cys	Asp 875	Thr	Val	Ala	Val	Lys	Met 880
Leu	Lys	Glu	Gly 885	Ala	Thr	Ala	Ser	Glu 890	His	Arg	Ala 895	Leu	Met	Ser	Glu

Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	Asn	His	Leu	Asn	Val	Val	Asn	Leu		
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			915				920						925				
Phe	Cys	Lys	Tyr	Gly	Asn	Leu	Ser	Asn	Phe	Leu	Arg	Ala	Lys	Arg	Asp		
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Ser	Asp	Arg	Val	Leu	Phe	Ala	Arg	Phe	Ser	Lys	Thr	Glu	Gly	Gly	Ala		
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Arg	Arg	Ala	Ser	Pro	Asp	Gln	Glu	Ala	Glu	Asp	Leu	Trp	Leu	Ser	Pro		
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Leu	Thr	Met	Glu	Asp	Leu	Val	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Arg	Gly		
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Arg	Asn	Ile	Leu	Leu	Ser	Glu	Ser	Asp	Val	Val	Lys	Ile	Cys	Asp	Phe		
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Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	Lys	Gly		
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Ser	Ala	Arg	Leu	Pro	Leu	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asp		
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Lys	Val	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu		
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Trp	Glu	Ile	Phe	Ser	Leu	Gly	Ala	Ser	Pro	Tyr	Pro	Gly	Val	Gln	Ile		
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Asn	Glu	Glu	Phe	Cys	Gln	Arg	Leu	Arg	Asp	Gly	Thr	Arg	Met	Arg	Ala		
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Pro	Glu	Leu	Ala	Thr	Pro	Ala	Ile	Arg	Arg	Ile	Met	Leu	Asn	Cys	Trp		
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Ser	Gly	Asp	Pro	Lys	Ala	Arg	Pro	Ala	Phe	Ser	Glu	Leu	Val	Glu	Ile		
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Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser
185 1190 1195 1200

Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp
1205 1210 1215

Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn
1220 1225 1230

Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly
1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr
1250 1255 1260

Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
265 1270 1275 1280

Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val Thr Arg Ala His
1300 1305 1310

Pro Asp Ser Gln Gly Arg Arg Arg Arg Pro Glu Arg Gly Ala Arg Gly
1315 1320 1325

Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu Ser Glu Pro Ser
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ccaccctgc ccccgccagc ggaccggtcc cccacccccg gtccttcac c atg cac 357
Met His
1

ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
5 10 15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
20 25 30

gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
35 40 45 50

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
55 60 65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
70 75 80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
85 90 95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
100 105 110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115 120 125 130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
135 140 145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
150 155 160

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg 885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
165 170 175

agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa 933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
180 185 190

00275439 - 031600

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Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
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tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
230 235 240	
tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct	1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tcg gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
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Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
295 300 305	
cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	
tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	
cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt	1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
390 395 400	
gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg	1605
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405 410 415	

003323-001500

420

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Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
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Gln Met Ser

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ttagagtgtc ttctaatttc aggtagaaga catgtccacc ttctgattat ttttgagaaa 180
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tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360
gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac      416
                                   Met Tyr
                                   1

aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg      464
Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
      5                                10                                15

gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag      512
Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
      20                                25                                30

tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg      560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
      35                                40                                45                                50

gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga      608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
      55                                60                                65

tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca      656
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
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tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca      704
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
      85                                90                                95

cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga      752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
      100                                105                                110

gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca      800
Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
      115                                120                                125                                130

ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc      848
Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys
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aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta	944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
165 170 175	
gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg	1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	
aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta	1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt	1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
340 345 350	
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tgccaagttg ctgtcactgt ttttttccca ggtgttaaaa aaaaaatcca ttttacacag 1585
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35 40 45
Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60
Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80
Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95
Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110
Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125
Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140
Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

00272999-03460
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Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
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Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
180 185 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
195 200 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
210 215 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225 230 235 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
260 265 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
290 295 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
305 310 315 320

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Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
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Asn Pro

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18

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009130-Share00

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Asn Ile Thr Glu Asp Ser Tyr Val Ile Asp Thr Gly Asp Ser Leu Ser
35 40 45

Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Thr Trp Pro Gly Ala
50 55 60

Gln Glu Val Leu Thr Thr Gly Gly Lys Asp Ser Glu Asp Thr Arg Val
65 70 75 80

Val	His	Asp	Cys	Glu	Gly	Thr	Glu	Ala	Arg	Pro	Tyr	Cys	Lys	Val	Leu
				85					90					95	

Leu Leu Ala Gln Thr His Ala Asn Asn Thr Gly Ser Tyr His Cys Tyr
100 105 110

Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Thr
115 120 125

Tyr Val Phe Val Arg Asp Phe Lys His Pro Phe Ile Asn Lys Pro Asp
130 135 140

Thr Leu Leu Val Asn Arg Lys Asp Ser Met Trp Val Pro Cys Leu Val
145 150 155 160

Ser	Ile	Pro	Gly	Leu	Asn	Ile	Thr	Leu	Arg	Ser	Gln	Ser	Ser	Ala	Leu
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His	Pro	Asp	Gly	Gln	Glu	Val	Leu	Trp	Asp	Asp	Arg	Arg	Gly	Met	Arg
				180				185				190			
Val	Pro	Thr	Gln	Leu	Leu	Arg	Asp	Ala	Leu	Tyr	Leu	Gln	Cys	Glu	Thr
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				210				215				220			
Thr	Gly	Asn	Glu	Leu	Tyr	Asp	Ile	Gln	Leu	Tyr	Pro	Lys	Lys	Ser	Met
225				230				235				240			
Glu	Leu	Leu	Val	Gly	Glu	Lys	Leu	Val	Leu	Asn	Cys	Thr	Val	Trp	Ala
				245				250				255			
Glu	Phe	Asp	Ser	Gly	Val	Thr	Phe	Asp	Trp	Asp	Tyr	Pro	Gly	Lys	Gln
				260				265				270			
Ala	Glu	Arg	Ala	Lys	Trp	Val	Pro	Glu	Arg	Arg	Ser	Gln	Gln	Thr	His
				275				280				285			
Thr	Glu	Leu	Ser	Ser	Ile	Leu	Thr	Ile	His	Asn	Val	Ser	Gln	Asn	Asp
				290				295				300			
Leu	Gly	Pro	Tyr	Val	Cys	Glu	Ala	Asn	Asn	Gly	Ile	Gln	Arg	Phe	Arg
305				310				315				320			
Glu	Ser	Thr	Glu	Val	Ile	Val	His	Glu	Lys	Pro	Phe	Ile	Ser	Val	Glu
				325				330				335			
Trp	Leu	Lys	Gly	Pro	Val	Leu	Glu	Ala	Thr	Ala	Gly	Asp	Glu	Leu	Val
				340				345				350			
Lys	Leu	Pro	Val	Lys	Leu	Ala	Ala	Tyr	Pro	Pro	Pro	Glu	Phe	Gln	Trp
				355				360				365			
Tyr	Lys	Asp	Arg	Lys	Ala	Val	Thr	Gly	Arg	His	Asn	Pro	His	Ala	Leu
				370				375				380			
Val	Leu	Lys	Glu	Val	Thr	Glu	Ala	Ser	Ala	Gly	Val	Tyr	Thr	Leu	Ala
385				390				395				400			
Leu	Trp	Asn	Ser	Ala	Ala	Gly	Leu	Arg	Gln	Asn	Ile	Ser	Leu	Glu	Leu
				405				410				415			
Val	Val	Asn	Val	Pro	Pro	His	Ile	His	Glu	Lys	Glu	Ala	Ser	Ser	Pro
				420				425				430			
Ser	Ile	Tyr	Ser	Arg	His	Ser	Arg	Gln	Thr	Leu	Thr	Cys	Thr	Ala	Tyr
				435				440				445			

Gly	Val	Pro	Gln	Pro	Leu	Ser	Val	Gln	Trp	His	Trp	Arg	Pro	Trp	Thr	
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Pro	Cys	Lys	Thr	Phe	Ala	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Arg	
465					470					475					480	
Asp	Gly	Met	Pro	Gln	Cys	Arg	Asp	Trp	Lys	Glu	Val	Thr	Thr	Gln	Asp	
				485					490					495		
Ala	Val	Asn	Pro	Ile	Glu	Ser	Leu	Asp	Ser	Trp	Thr	Glu	Phe	Val	Glu	
			500					505					510			
Gly	Lys	Asn	Lys	Thr	Val	Ser	Lys	Leu	Val	Ile	Gln	Asp	Ala	Asn	Val	
			515				520					525				
Ser	Ala	Met	Tyr	Lys	Cys	Val	Val	Val	Asn	Lys	Val	Gly	Gln	Asp	Glu	
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Arg	Leu	Ile	Tyr	Phe	Tyr	Val	Thr	Thr	Ile	Pro	Asp	Gly	Phe	Ser	Ile	
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Glu	Ser	Glu	Pro	Ser	Glu	Asp	Pro	Leu	Glu	Gly	Gln	Ser	Val	Arg	Leu	
				565					570					575		
Ser	Cys	Arg	Ala	Asp	Asn	Tyr	Thr	Tyr	Glu	His	Leu	Arg	Trp	Tyr	Arg	
			580					585					590			
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Pro	Arg	Val	Ala	Pro	Glu	Asp	Glu	Gly	Asp	Tyr	Val	Cys	Glu	Val	Gln	
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675							680					685				
Val	Asn	Val	Ser	Asp	Ser	Leu	Glu	Met	Arg	Cys	Pro	Val	Ala	Gly	Ala	
690						695					700					
His	Val	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Lys	
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Glu	Ser	Gly	Ile	Asp	Leu	Ala	Asp	Ser	Asn	Gln	Arg	Leu	Ser	Ile	Gln	
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Arg	Val	Arg	Glu	Glu	Asp	Ala	Gly	Arg	Tyr	Leu	Cys	Ser	Val	Cys	Asn	
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Ala	Lys	Gly	Cys	Val	Asn	Ser	Ser	Ala	Ser	Val	Ala	Val	Glu	Gly	Ser	
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Glu	Asp	Lys	Gly	Ser	Met	Glu	Ile	Val	Ile	Leu	Ile	Gly	Thr	Gly	Val	
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Ile	Ala	Val	Phe	Phe	Trp	Val	Leu	Leu	Leu	Leu	Ile	Phe	Cys	Asn	Met	
785					790					795					800	
Lys	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Ile	
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Arg Asn Ile Leu Leu Ser Glu Ser Asp Ile Val Lys Ile Cys Asp Phe
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Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
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Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp
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Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu
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Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile
1105 1110 1115 1120

Asn Glu Glu Phe Cys Gln Arg Leu Lys Asp Gly Thr Arg Met Arg Ala
1125 1130 1135

Pro Glu Leu Ala Thr Pro Ala Ile Arg His Ile Met Gln Ser Cys Trp
1140 1145 1150

Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Asp Leu Val Glu Ile
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Leu Gly Asp Leu Leu Gln Gly Gly Gly Trp Gln Glu Glu Glu Glu
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Arg Met Ala Leu His Ser Ser Gln Ser Ser Glu Glu Asp Gly Phe Met
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Gln Ala Ser Thr Thr Ala Leu His Ile Thr Glu Ala Asp Ala Asp Asp
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Ser Pro Pro Ser Met His Cys His Ser Leu Ala Ala Arg Tyr Tyr Asn
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Cys Val Ser Phe Pro Gly Arg Leu Ala Arg Gly Thr Lys Thr Pro Gly
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Ser Ser Arg Met Lys Thr Phe Glu Glu Leu Pro Met Thr Pro Thr Thr
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Tyr Lys Ala Ser Met Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
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Ser Glu Glu Phe Glu Glu Leu Glu Ser Arg His Arg Pro Glu Gly Ser
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